

TOH CENTER 1600/2900

RAW SEQUENCE LISTING PATENT APPLICATION: US/09/730,465

SEQUENCE LISTING

DATE: 06/06/2001 TIME: 12:26:38

Input Set : A:\10274-006002.txt Output Set: C:\CRF3\06062001\1730465.raw

ENTERED

SEQUENCE LISTING			
4 (1) GENERAL INFORMATION:			
C>	6	(i)	APPLICANT: Wallner, Barbara P.
	7		Cooper, Kevin D.
	9	(ii)	TITLE OF INVENTION: Method of Prophylaxis or Treatment of Antigen
	10		Presenting Cell Driven Skin Conditions Using
	11		Inhibitors of the CD2/LFA-3 Interaction
	13	(iii)	NUMBER OF SEQUENCES: 8
	15	(iv)	CORRESPONDENCE ADDRESS:
	16		(A) ADDRESSEE: LAHIVE & COCKFIELD
	17		(B) STREET: 60 State Street, Suite 510
	18		(C) CITY: Boston
	19		(D) STATE: Massachusetts
	20		(E) COUNTRY: USA
	21		(F) ZIP: 02109-1875
	23	(v)	COMPUTER READABLE FORM:
	24	,	(A) MEDIUM TYPE: Floppy disk
	25		(B) COMPUTER: IBM PC compatible
	26		(C) OPERATING SYSTEM: PC-DOS/MS-DOS
	27		(D) SOFTWARE: PatentIn Release #1.0, Version #1.25
	29	(vi)	CURRENT APPLICATION DATA:
C>	30	, ,	(A) APPLICATION NUMBER: US/09/730,465
C>			(B) FILING DATE: 05-Dec-2000
	41	(vii)	PRIOR APPLICATION DATA:
	34		(A) APPLICATION NUMBER: PCT/US92/08755
	35		(B) FILING DATE: 06-OCT-1992
	38		(A) APPLICATION NUMBER: US 07/862,022
	39		(B) FILING DATE: 12-APR-1992
	42		(A) APPLICATION NUMBER: US 07/770,969
	43		(B) FILING DATE: 07-OCT-1991
	45	(viii)	ATTORNEY/AGENT INFORMATION:
	46		(A) NAME: Myers, Louis (PLM)
	47		(B) REGISTRATION NUMBER: 35,965
	48		(C) REFERENCE/DOCKET NUMBER: BGP-111CP
	50	(ix)	TELECOMMUNICATION INFORMATION:
	51		(A) TELEPHONE: (617)227-7400
	52		(B) TELEFAX: (617)227-5941
	55	(2) INFO	RMATION FOR SEQ ID NO: 1:
	57	(i)	SEQUENCE CHARACTERISTICS:
	58		(A) LENGTH: 753 base pairs
	59		(B) TYPE: nucleic acid
	60		(C) STRANDEDNESS: single
	61		(D) TOPOLOGY: linear
	63	(ii)	MOLECULE TYPE: cDNA
	66	(ix)	FEATURE:
	67		(A) NAME/KEY: CDS

(B) LOCATION: 1..750

68

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Input Set : A:\10274-006002.txt
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70 (ix) FEATURE:	
71 (A) NAME/KEY: sig_peptide	
72 (B) LOCATION: 184	
74 (ix) FEATURE:	
75 (A) NAME/KEY: mat_peptide	
76 (B) LOCATION: 85750	
78 (ix) FEATURE:	
79 (A) NAME/KEY: misc_feature	
80 (B) LOCATION: 1750	
81 (D) OTHER INFORMATION: /note= "Human transmembrane LFA-3"	
83 (ix) FEATURE:	
84 (A) NAME/KEY: misc feature	
85 (B) LOCATION: 646	
86 (D) OTHER INFORMATION: /note= "Transmembrane domain"	
89 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:	
91 ATG GTT GCT GGG AGC GAC GCG GGG CGG GCC CTG GGG GTC CTC AGC GTG	48
92 Met Val Ala Gly Ser Asp Ala Gly Arg Ala Leu Gly Val Leu Ser Val	
93 -28 -25 -20 -15	
95 GTC TGC CTG CAC TGC TTT GGT TTC ATC AGC TGT TTT TCC CAA CAA	96
96 Val Cys Leu Leu His Cys Phe Gly Phe Ile Ser Cys Phe Ser Gln Gln	90
97 -10 -5 1	
	144
99 ATA TAT GGT GTT GTG TAT GGG AAT GTA ACT TTC CAT GTA CCA AGC AAT	144
100 Ile Tyr Gly Val Val Tyr Gly Asn Val Thr Phe His Val Pro Ser Asn	
101 5 10 15 20	
103 GTG CCT TTA AAA GAG GTC CTA TGG AAA AAA CAA AAG GAT AAA GTT GCA	192
104 Val Pro Leu Lys Glu Val Leu Trp Lys Lys Gln Lys Asp Lys Val Ala	
105 25 30 35	
107 GAA CTG GAA AAT TCT GAA TTC AGA GCT TTC TCA TCT TTT AAA AAT AGG	240
108 Glu Leu Glu Asn Ser Glu Phe Arg Ala Phe Ser Ser Phe Lys Asn Arg	
109 40 45 50	
111 GTT TAT TTA GAC ACT GTG TCA GGT AGC CTC ACT ATC TAC AAC TTA ACA	288
112 Val Tyr Leu Asp Thr Val Ser Gly Ser Leu Thr Ile Tyr Asn Leu Thr	
113 55 60 65	
115 TCA TCA GAT GAA GAT GAG TAT GAA ATG GAA TCG CCA AAT ATT ACT GAT	336
116 Ser Ser Asp Glu Asp Glu Tyr Glu Met Glu Ser Pro Asn Ile Thr Asp	
117 70 75 80	
119 ACC ATG AAG TTC TTT CTT TAT GTG CTT GAG TCT CTT CCA TCT CCC ACA	384
120 Thr Met Lys Phe Phe Leu Tyr Val Leu Glu Ser Leu Pro Ser Pro Thr	
121 85 90 95 100	
123 CTA ACT TGT GCA TTG ACT AAT GGA AGC ATT GAA GTC CAA TGC ATG ATA	432
124 Leu Thr Cys Ala Leu Thr Asn Gly Ser Ile Glu Val Gln Cys Met Ile	
125 105 110 115	
127 CCA GAG CAT TAC AAC AGC CAT CGA GGA CTT ATA ATG TAC TCA TGG GAT	480
128 Pro Glu His Tyr Asn Ser His Arg Gly Leu Ile Met Tyr Ser Trp Asp	
129 120 125 130	
131 TGT CCT ATG GAG CAA TGT AAA CGT AAC TCA ACC AGT ATA TAT TTT AAG	528
132 Cys Pro Met Glu Gln Cys Lys Arg Asn Ser Thr Ser Ile Tyr Phe Lys	
133 135 140 145	
135 ATG GAA AAT GAT CTT CCA CAA AAA ATA CAG TGT ACT CTT AGC AAT CCA	576
100 mil out out out out that mil out out has out how out	0.0

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136 Met Glu Asn Asp Leu Pro Gln Lys Ile Gln Cys Thr Leu Ser Asn Pro
137 150 155
139 TTA TTT AAT ACA ACA TCA TCA ATC ATT TTG ACA ACC TGT ATC CCA AGC
                                                                  624
140 Leu Phe Asn Thr Thr Ser Ser Ile Ile Leu Thr Thr Cys Ile Pro Ser
                    170
                                     175
143 AGC GGT CAT TCA AGA CAC AGA TAT GCA CTT ATA CCC ATA CCA TTA GCA
                                                                  672
144 Ser Gly His Ser Arg His Arg Tyr Ala Leu Ile Pro Ile Pro Leu Ala
                 185
                                   190
147 GTA ATT ACA ACA TGT ATT GTG CTG TAT ATG AAT GGT ATT CTG AAA TGT
                                                                  720
148 Val Ile Thr Thr Cys Ile Val Leu Tyr Met Asn Gly Ile Leu Lys Cys
                               205
151 GAC AGA AAA CCA GAC AGA ACC AAC TCC AAT TGA
                                                                  753
152 Asp Arg Lys Pro Asp Arg Thr Asn Ser Asn
153 215 220
156 (2) INFORMATION FOR SEO ID NO: 2:
158 (i) SEQUENCE CHARACTERISTICS:
159
            (A) LENGTH: 250 amino acids
            (B) TYPE: amino acid
160
            (D) TOPOLOGY: linear
161
      (ii) MOLECULE TYPE: protein
163
      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:
167 Met Val Ala Gly Ser Asp Ala Gly Arq Ala Leu Gly Val Leu Ser Val
168 -28 -25
                               -20
170 Val Cys Leu Leu His Cys Phe Gly Phe Ile Ser Cys Phe Ser Gln Gln
171 -10
                            -5
173 Ile Tyr Gly Val Val Tyr Gly Asn Val Thr Phe His Val Pro Ser Asn
                     10
                                       1.5
176 Val Pro Leu Lys Glu Val Leu Trp Lys Lys Gln Lys Asp Lys Val Ala
                 25
                                   30
179 Glu Leu Glu Asn Ser Glu Phe Arg Ala Phe Ser Ser Phe Lys Asn Arg
             4.0
                                45
182 Val Tyr Leu Asp Thr Val Ser Gly Ser Leu Thr Ile Tyr Asn Leu Thr
183 55
                            60
185 Ser Ser Asp Glu Asp Glu Tyr Glu Met Glu Ser Pro Asn Ile Thr Asp
                         75
188 Thr Met Lys Phe Phe Leu Tyr Val Leu Glu Ser Leu Pro Ser Pro Thr
                     90
                                       95
191 Leu Thr Cys Ala Leu Thr Asn Gly Ser Ile Glu Val Gln Cys Met Ile
                 105
                                   110
194 Pro Glu His Tyr Asn Ser His Arg Gly Leu Ile Met Tyr Ser Trp Asp
195 120
                               125
197 Cys Pro Met Glu Gln Cys Lys Arg Asn Ser Thr Ser Ile Tyr Phe Lys
198 135
                            140
                                 145
200 Met Glu Asn Asp Leu Pro Gln Lys Ile Gln Cys Thr Leu Ser Asn Pro
201 150
                        155
203 Leu Phe Asn Thr Thr Ser Ser Ile Ile Leu Thr Thr Cys Ile Pro Ser
204 165 170
                            175
206 Ser Gly His Ser Arg His Arg Tyr Ala Leu Ile Pro Ile Pro Leu Ala
                                   190
                185
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RAW SEQUENCE LISTING PATENT APPLICATION: US/09/730.465 DATE: 06/06/2001 TIME: 12:26:38

Input Set : A:\10274-006002.txt
Output Set: C:\CRF3\06062001\I730465.raw

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209 Val Ile Thr Thr Cvs Ile Val Leu Tvr Met Asn Glv Ile Leu Lvs Cvs
               200
                                    205
210
212 Asp Arg Lys Pro Asp Arg Thr Asn Ser Asn
213
            215
                                220
215 (2) INFORMATION FOR SEQ ID NO: 3:
       (i) SEQUENCE CHARACTERISTICS:
217
              (A) LENGTH: 723 base pairs
218
219
              (B) TYPE: nucleic acid
220
              (C) STRANDEDNESS: single
221
              (D) TOPOLOGY; linear
223
       (ii) MOLECULE TYPE: cDNA
226
       (ix) FEATURE:
              (A) NAME/KEY: CDS
227
228
              (B) LOCATION: 1..720
230
        (ix) FEATURE:
231
              (A) NAME/KEY: sig peptide
232
              (B) LOCATION: 1..84
234
       (ix) FEATURE:
235
              (A) NAME/KEY: mat peptide
              (B) LOCATION: 85..720
       (ix) FEATURE:
              (A) NAME/KEY: misc feature
              (B) LOCATION: 1..720
241
              (D) OTHER INFORMATION: /note= "Human PI-linked LFA-3"
243
       (ix) FEATURE:
              (A) NAME/KEY: misc feature
              (B) LOCATION: 568..720
              (D) OTHER INFORMATION: /note= "Signal sequence for
247 PI-linkage"
      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:
252 ATG GTT GCT GGG AGC GAC GCG GGG CGG GCC CTG GGG GTC CTC AGC GTG
253 Met Val Ala Gly Ser Asp Ala Gly Arg Ala Leu Gly Val Leu Ser Val
254 -28
              -25
                                    -20
256 GTC TGC CTG CTG CAC TGC TTT GGT TTC ATC AGC TGT TTT TCC CAA CAA
257 Val Cys Leu Leu His Cys Phe Gly Phe Ile Ser Cys Phe Ser Gln Gln
           -10
                                 -5
260 ATA TAT GGT GTT GTG TAT GGG AAT GTA ACT TTC CAT GTA CCA AGC AAT
261 Ile Tyr Gly Val Val Tyr Gly Asn Val Thr Phe His Val Pro Ser Asn
                         10
                                             15
264 GTG CCT TTA AAA GAG GTC CTA TGG AAA AAA CAA AAG GAT AAA GTT GCA
                                                                           192
265 Val Pro Leu Lys Glu Val Leu Trp Lys Lys Gln Lys Asp Lys Val Ala
                     25
                                         30
268 GAA CTG GAA AAT TCT GAA TTC AGA GCT TTC TCA TCT TTT AAA AAT AGG
269 Glu Leu Glu Asn Ser Glu Phe Arg Ala Phe Ser Ser Phe Lys Asn Arg
                40
                                     45
272 GTT TAT TTA GAC ACT GTG TCA GGT AGC CTC ACT ATC TAC AAC TTA ACA
                                                                           288
273 Val Tyr Leu Asp Thr Val Ser Gly Ser Leu Thr Ile Tyr Asn Leu Thr
            55
                                 60
276 TCA TCA GAT GAA GAT GAG TAT GAA ATG GAA TCG CCA AAT ATT ACT GAT
```

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```
277 Ser Ser Asp Glu Asp Glu Tyr Glu Met Glu Ser Pro Asn Ile Thr Asp
278 70
                          75
280 ACC ATG AAG TTC TTT CTT TAT GTG CTT GAG TCT CTT CCA TCT CCC ACA
                                                                    384
281 Thr Met Lys Phe Phe Leu Tyr Val Leu Glu Ser Leu Pro Ser Pro Thr
                      90
                                        95
284 CTA ACT TGT GCA TTG ACT AAT GGA AGC ATT GAA GTC CAA TGC ATG ATA
                                                                    432
285 Leu Thr Cys Ala Leu Thr Asn Gly Ser Ile Glu Val Gln Cys Met Ile
                  105
                                    110
288 CCA GAG CAT TAC AAC AGC CAT CGA GGA CTT ATA ATG TAC TCA TGG GAT
289 Pro Glu His Tyr Asn Ser His Arg Gly Leu Ile Met Tyr Ser Trp Asp
             120
                                125
292 TGT CCT ATG GAG CAA TGT AAA CGT AAC TCA ACC AGT ATA TAT TTT AAG
                                                                    528
293 Cys Pro Met Glu Gln Cys Lys Arg Asn Ser Thr Ser Ile Tyr Phe Lys
                             140
296 ATG GAA AAT GAT CTT CCA CAA AAA ATA CAG TGT ACT CTT AGC AAT CCA
                                                                    576
297 Met Glu Asn Asp Leu Pro Gln Lys Ile Gln Cys Thr Leu Ser Asn Pro
                         155
300 TTA TTT AAT ACA ACA TCA TCA ATC ATT TTG ACA ACC TGT ATC CCA AGC
                                                                    624
301 Leu Phe Asn Thr Thr Ser Ser Ile Ile Leu Thr Thr Cys Ile Pro Ser
                     170
                                        175
304 AGC GGT CAT TCA AGA CAC AGA TAT GCA CTT ATA CCC ATA CCA TTA GCA
                                                                    672
305 Ser Gly His Ser Arg His Arg Tyr Ala Leu Ile Pro Ile Pro Leu Ala
                                  190
                 185
308 GTA ATT ACA ACA TGT ATT GTG CTG TAT ATG AAT GGT ATG TAT GCT TTT
                                                                    720
309 Val Ile Thr Thr Cys Ile Val Leu Tyr Met Asn Gly Met Tyr Ala Phe
                                 205
           200
312 TAA
                                                                    723
315 (2) INFORMATION FOR SEQ ID NO: 4:
317 (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 240 amino acids
318
319
            (B) TYPE: amino acid
320
            (D) TOPOLOGY: linear
      (ii) MOLECULE TYPE: protein
322
      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:
326 Met Val Ala Gly Ser Asp Ala Gly Arg Ala Leu Gly Val Leu Ser Val
327 -28 -25 -20 -15
329 Val Cys Leu Leu His Cys Phe Gly Phe Ile Ser Cys Phe Ser Gln Gln
330 -10
                      -5
332 Ile Tyr Gly Val Val Tyr Gly Asn Val Thr Phe His Val Pro Ser Asn
                      10
                                        15
335 Val Pro Leu Lys Glu Val Leu Trp Lys Lys Gln Lys Asp Lys Val Ala
                  25
                                     30
338 Glu Leu Glu Asn Ser Glu Phe Arg Ala Phe Ser Ser Phe Lys Asn Arg
339 40
                                 45
341 Val Tyr Leu Asp Thr Val Ser Gly Ser Leu Thr Ile Tyr Asn Leu Thr
342 55
                             60
344 Ser Ser Asp Glu Asp Glu Tyr Glu Met Glu Ser Pro Asn Ile Thr Asp
345 70
347 Thr Met Lys Phe Phe Leu Tyr Val Leu Glu Ser Leu Pro Ser Pro Thr
```

VERIFICATION SUMMARY

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DATE: 06/06/2001 TIME: 12:26:39

Input Set : A:\10274-006002.txt

Output Set: C:\CRF3\06062001\1730465.raw

L:6 M:220 C: Keyword misspelled or invalid format, [(i) APPLICANT:]

L:30 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]

L:31 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]